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FIGURE 1A

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423 AAC N	477 TGC C	531 TGT C	585 ATT I	639 ACC T	693 ATA I	747 GTG
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AGC	AAT N	CCC	GTG V	AGT	TTC	GAA
CAG Q	GAG	999	CAC H	GAG	CTC	GAG
405 TGC C	459 ACT T	513 ATG M	567 GGA G	621 ACA T	675 GTC V	729 ACA
TGC	CTT	TGC	TCT	GCT	AAT N	TGA
TTC F	AAT N	AAA K	TTA L	TGT C	ACC	ATC
396 TCC S	450 ACC T	504 GAC D	558 TCC S	612 GGC G	999 999	720 GCT
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ACC	CCC	TTC	TGC	ATG M	CCC	TGA
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CAC ATG H M	TCT	GCG A	AAC N	TTT F	GAA E	TCC
CAC H	TTG	ACT	GAA	603 AGA TTT GCT A R F A M	GCT	711 CAC TCC CCC H S P

FIGURE 1B

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FIGURE 1C

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Figure 2B

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Figure 2C

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Figure 2D

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Figure 2E

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Figure 2F

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Figure 2G

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Figure 2H

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Figure 2I

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Figure 2J

consensus	8941	10033	T0644	10774	71854	72861	74452	155045		619856	683480	1291208	•	consensus	8941	10033	10644	10774	71854	72861	74452	155045	156817	619856	683480	1291208		
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32%	262 589 185	151 255 174	721	252 241	751 322 324	262 262 619 185 185	279	751	252 241

Figure 2M

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consensus 8941	10033 10644 10774 71854	72861 74452	155045 156817 610066	683480 1291208	consensus 8941	10033 10644 10774	71854 72861 74452	155045 156817 619856 683480	1291208
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781 327 324	262 649 185	298	781	252 247	810 327	324 262 678	185 151 318	174 810 224 252	250

Figure 2N

GIPL aa TFLLAFVLLCTLLGLGCPLHCE-YLHTICLLFIFVARGNSRSCD 口 ı R P MRLSR 7

g

GIPL aa I C T A A G S R C H G Q M K T C S S D K D T C V L L V G K A F C H N I G K D C D G Y E E E C S S P E D V C G K V L L E I

GIPL aa KGKELVHTYKGCIRSQDCYSGVISTMG ASLSVRTVHKNCFSSSICKLGQFDVNIG S K G S FS 여정

GIPL aa gg DHMVTSSFCCQSDGCNS-AFLSVPLTNL SYIRGRINCCEKELCEDOPFPGLPLSK-PKDHMVT HH 8 8

GIPL aa B THCTGKEN AICKGTET TENGLMCPACTASFRDKCMGPM-PNGYYCPGAIGLFTKDSTEYE 120 113

GIPL aa SM ı 1 HCVSLSGHVQAGIFKP--RFAMRGCATE KCINIVGH-RYEOFFGDISYNLKGCVSS 150 142

GIPL aa LA IR Д TKPGAEVPTGTNVLFLHHIECTHS LLSLSNATFEONRNYLEKVECKDA CPLLSLSNAT 169 178

S 199

GIPL aa g

gg

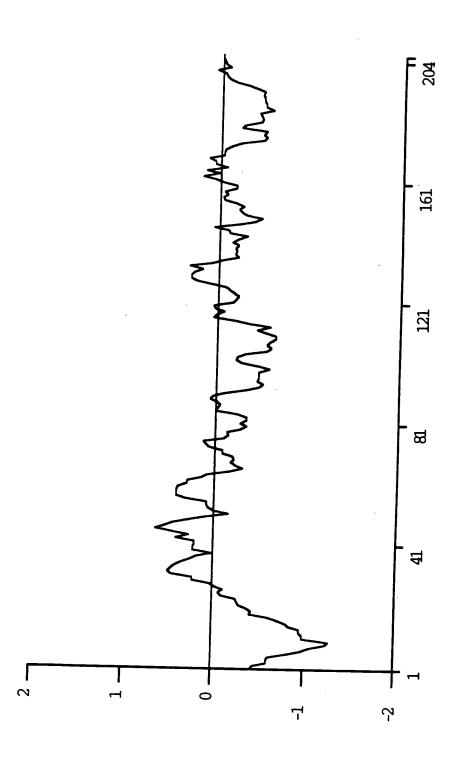
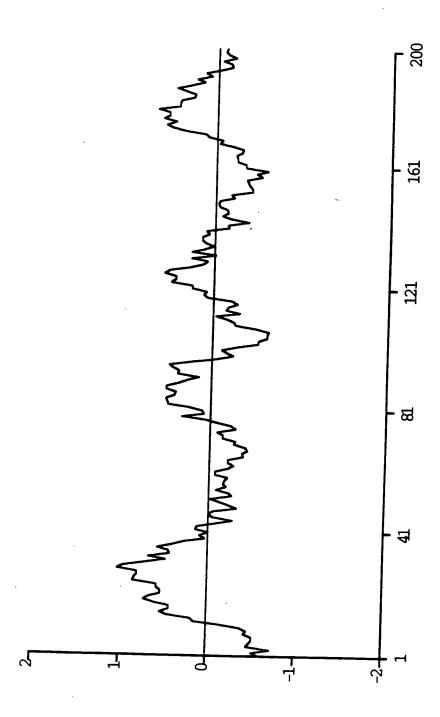


FIGURE 4



FIGURE!

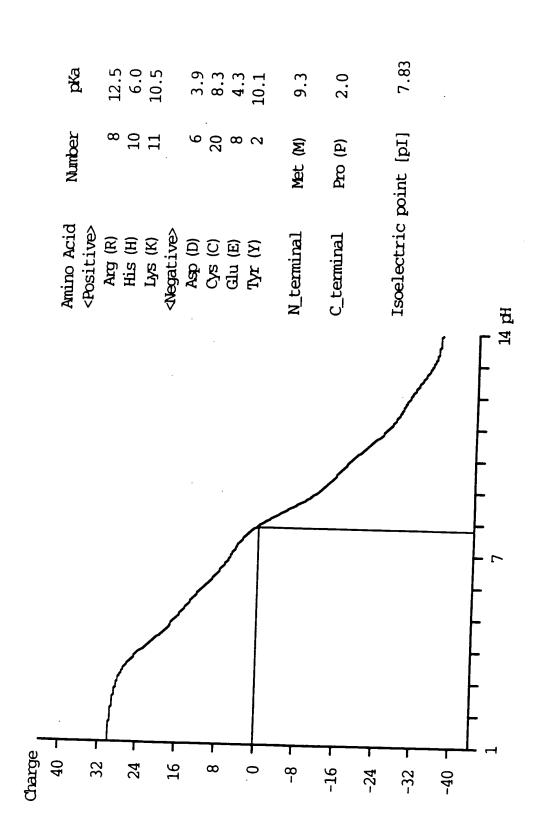


FIGURE 6

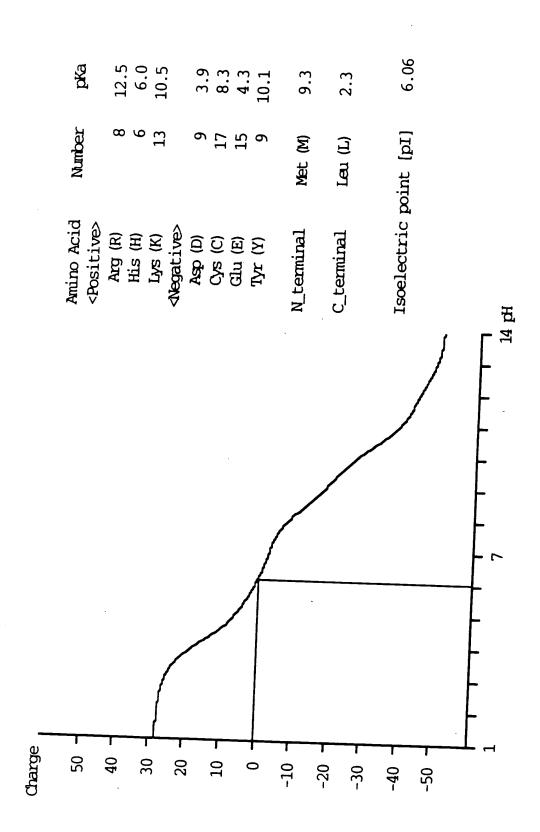


FIGURE 7

13 27 5' NCA ATG GGC CGG CGG TGG GAA GGG TGA ATG TGG GTC CAG ACC CGC CCC TCC TCA 72 GCT TCC TAT AAA AGC TGG GGA CCA GGT ACT GCT GAT ACA CAC ACC ATG AGG CTC 117 126 135 TCC AGG AGA CCA GAG ACC TIT CTG CTG GCC TIT GTG TTG CTC TGC ACC CTC CTG SRRPETFLLAFVLLCT 171 130 GGT CTT GGG TGC CCA CTA CAC TGC GAA ATA TGT ACG GCG GCG GGG AGC AGC TGC G L G C P L H C E I C T A A G S R C 189 234 243 CAT GGC CAA ATG AAG ACC TOC AGC AGT GAC AAG GAC ACA TOT GTG CTC CTG GTC H G Q M K T C S S D K D T C V L L V 297 GGG AAG GCT ACT TCA AAG GGC AAG GAG TTG GTG CAC ACC TAC AAG GGC TGC ATC GKATSKGKELVHTYKGCI 342 351 AGG TOO CAG GAC TGC TAC TOO GGC GTT ATA TOO ACC ACC ATG GGC CCC AAG GAC CYSGVISTTMGPKD 387 396 405 CAC ATG GTA ACC AGC TCC TTC TGC TGC CAG AGC GAC GGC TGC AAC AGT GCC TTT H M V T S S F C C Q S D G C N S A F 450 459 TTG TOT GIT COO TTG ACC AAT CIT ACT GAG AAT GGO CTG ATG TGC CCC GCC TGC 468 LSVPLTNLTENGLM 495 504 513 . ACT GCG AGC TTC AGG GAC AAA TGC ATG GGG CCC ATG ACC CAC TGT ACT GGA AAG 522 ASFRDKCMGPMTHCTGK

558 567 576 585 GAA AAC CAC TGC GTC TCC TTA TCT GGA CAC GTG CAG GCT GGT ATT TTC AAA CCC ENHCVSLSGHVQAGIFKP 621 630 612 539 AGA TIT GCT ATG CGG GGC TGT GCT ACA GAG AGT ATG TGC TTT ACC AAG CCT GGT R F A M R G C A T E S M C F T K P G 693 666 675 684 GCT GAA GTA CCC ACA GGC ACC AAT GTC CTC TTC CTC CAT CAT ATA GAG TGC ACT A E V P T G T N V L F L H H I E C T 720 729 CAC TOO COO TGA AAA GOT ATC TGA ACA GAG GAA GAT AAT GTA GTG TGA AGT COO H S P 783 CAT TIG TCC TCA GCC TGT AAC TTC CCC GTG TGC CTA TAA AGA AGT TAA TAG AGC AAA AAA AAA AAA AAA AAA AAA AAC TOG AG 3'

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NCAATGGGCCGGCCGTGGGAAGGGTGAATG 156817
   A G A A A G A G A C C A T N C C A G G A A - - G T - - - T G 619856
                                             583480
                       ---GGAA--
   TGGGTCCAGACCCGCCCCTCCTCAGCTTCC
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   TATAAAAGCTGGGGACCAGGTACTGCTGAT consensus
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         AAGCTGGGGACCAGGTACTGCTGAT 156817
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121 GAGACCTTTCTGCTGGCCTTTGTGTTGCTC consensus
                                  3941
                                 10033
                 GGCCTTTGTGTTGCTC
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1
151 TGCACCCTCCTGGGTCTTGGGTGCCCACTA consensus
  TNCACCCTCCTGGGTCTTGGGTGCCCACTA 10033
  TGCACCCTCCTGGGTCTTGGGTGCCCACTA 10774
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    CACCCTCCNGGGTCTNGGGTGCCCACNA 155045
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  CACTGCGAAATATGTACGGCGGGGGAGC
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  C A C T G C G A A N T A T G T A C G G C G G G G T A G C
 CACTGCGAAATATGTACGGCGGGGGGGC
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  NNNNNNCAATGGGC-CGGCCGTGGGAAG- 1291208
71
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```
211 AGGTGCCATGGCCAAATGAAGACC
                                                                         TGCAGC
                               GGTCAGC---
                                                                         --CAGC
                                                                                         8941
                                     CCAAATGAAGACCTGCAGC 10033
2
79
                                          AAATGAAGACCT
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                T C C A T G N C C A A A T N A A G A N C T T C A N C 155045
G C C A T G G C C A A A T G A A G A C C T G C A G C 156817
- - - T G G T C A G C - - - - - - - - C A G C 619856
G - - - - - - A A T G T G G G T C - - C A G - 1291208
79
211
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99
```

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241 AGTGACAAGGACACATGTGTGCTCCTGGTC consensus
   ACTGTC------CCTGCCTGTCCCCA-TC 3941
   AGTGACAAGGACACATGTGTGCTCCTGGTC 10033
   -----ACACATGTGTNCTCCTGGTC 10644
109 AGTGACAAGGACACATGTGTGCTCCTGGTC 10774
109 NGTGACAAGGACACATGTNTGCTCCTGGTC
241 AGTGACAAGGACACATGTGTGCTCCTGGTC
                 - C C T G C C T G T C C C C A - T C 619856
                    - - A C C C G C C C C T C C T C 1291208
271 GGGAAGGCTACTTCAAAGGGCAAGGAGTTG consensus
   128 GGGAAGGCTACTTCAAAGGGCAAGGAGTTG 10033
   GGGAAGGCTACTTCAAAGGGCAAGGAGTTG 10644
139 GGGAAGGCTACTTCAAAGGGCAAGGAGTTG 10774
                                       71854
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1
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139 GGNAAGNCTACTTCAAAGGGCAAGGAGTTG
271 GGGAAGGCTACTTCAAAGGGCAAGGAGTTG
        -- CCA---CAGAGGGCAAGGAGTTG 619856
       -----GTTG 683480
130 A G - - - - - - C T T C - - - - -
301 GTGCACACCTACAAGGGCTGCATCAGGTCC consensus
105 GTGCACCTACAAGGGCTGCATCAGGTCC
  GTGCACACCTACAAGGGCTGCATCAGGTCC 10033
158
52
  G T G C A C A C C T A C A A G G G C T G C A T C A G G T N C
159 GTGCACACCTACAAGGGCTGCATCAGGTCC
3
5
  G T G C A C A C C T A C A A G G G C T G C A T C A G G T C C
                                       74452
159 GTGCAC
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301 GTGCACACCTACAAGGGCTGCATCAGGTCC 156817
  GTGCACAACTACAAGGGCTGCATCAGGTCC
  G T G C A C A C C T A C A A G G G C T G C A T C A G G T C C
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351 ACCATGGGCCCCAAGGACCACATGGTAACC consensus
 155 ACCATGGGCCCCAAGGACCACATGGTAACC 8941
   ACCATGGGECCCAAGGACCACATGGTAACC 10033
   A C C A T G G G C C C A A G G A C C A C A T G G T A A C C
 112
   ACCATGGGCCCCAAGGACCACATGGTAACC
 229
                                          10774
   A C C A T G G G C C C A A G G A C C A C A T G G T A A C C
   ACCATGGGCCCAAGGACCACATGGTAACC
 55
   ACCATGGGCCCAAGGACCACATGGTAACC
 20
                                          74452
 174
                                          155045
351 ACCATGGGCCCCAAGGACCACATGGTAACC
                                          156817
   ACCATGGGCCCCAAGGACCACATGGT
199
                                          519856
   ACCATGGGNCCCAAGGACCACATGGTAACC
55
                                          683480
             ----GGGACCA---GGTA---
                                          1291208
   AGCTCCTTCTGCTGCCAGAGCGACGGCTGC consensus
391
   AGCTCCTTCTGNTGCCAGAGCGACGGCTGC 8941
   AGCTCCTTCTGCTGC-AGAGCGACGGCTGC
   AGCTCCTTCTGCTGCCAGAGCGACGGCTGC 10644
  AGCTCCTTCTGCTGCCAGAGCGACGGCTGC
259
                                          10774
   AGCTCCTTCTGCTGCCAGAGCGACGGCTGC
50
                                          71854
   AGCTCCTTNTGCTGCCAGAGCGACGGCTGC
95
                                          72861
   AGCTCCTTCTGCTGCCAGAGCGACGGCTGC
50
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   AGCTCCTTCTGCTGCCAGAGCGACGGCTGC
391
                                         156817
224
                                          619856
   A G C T C C T T N T G C T G C C A G A G C G A C G N C T G C
95
  AACAGTGCCTTTTTGTCTGTTCCCTTGACC
421
                                         consensus
  AACAGTGCCTTTTTGTCTGTTCCCTTGACC
225
                                          8941
  A A C A G T G C C T T T T T G T C T G T T C C C T T G A C C
277
                                         10033
  AACAGTGCCTTTTTGTCTGTTCCCTTGACC
172
                                         10644
  AACAGTGCCTT
289
                 TTTGTCTGTTCCCTTGACC
                                         10774
  AACANTGCC
              TT
                 TTTNTNTGTTCCCTTGACC
  AACATTGCCTTTTTNTNTGTNCCCTTG
125
  AACANTGCCTTTTTNTNTGTTCCCTTGACC
80
                                         74452
174
                                          155045
421
  AACAGTGCCTTTTTGTCTGTTCCCTTGACC 156817
224
                                          619856
125
  AACAGTGCCT
                  TTGTCTGTTCCCTTGACC 683480
```

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A A T C T T A C T G A G A A T G G C C T G A T G T G C C C Consensus
  AATCTTACTGAGAATGGCCTGATGTGCCCN 8941
  AATCTTACTGAGAATGGT
                                           10033
202 AATNTTACTGAGAATNGNCTGATGCCCC
                                          10644
319 AATCTTACTGAGAATGGCCTGATGTGCCCC
                                          10774
                                          71854
151
                                          72861
110 AATCTTACTGAGAATGGCCTGATGTGCCCC
                                          74452
174
                                          155045
  AATCTTACTGAGAATGGCCTGATGTGCCCC
451
                                          156817
224
                                          619856
  AATCTTACTGAGAATGGCCTGATGTGCCCC
155
                                          683480
153
                      ----TGATACAC---
```

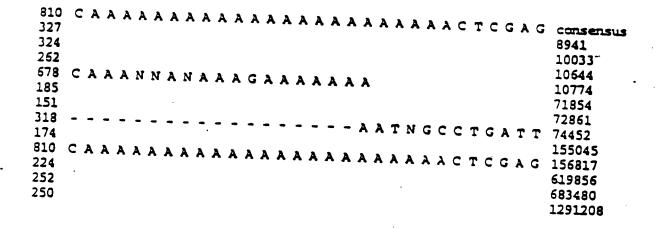
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431 GCCTGCACTGCGAGCTTCAGGGACAAATGC consensus
 235 GC-TGCACTGCGAGTTTNAGGGNCAAA--- 3941
   GNCTGCACTGNGAGCTTCAGGGACAAATGC
 232
                                         10033
 349 GCCTGCACTGCGAGCTTCAGGGACAAATGC 10774
 140 GCCTGCACTGCGAGCTTCAGGGACAAATGC
                                         71854
 140 GCCTGCACTGCGAGCTTCAGGGACAAATGC 74452
 481 GCCTGCACTGCGAGCTTCAGGGACAAATGC 156817
 185 GNCTGCACTGCGAGCTTNAGGGACAAATGC
   ----ACAC-----
                                        683480
 511 ATGGGGCCCATGACCCACTGTACTGGAAAG
 324
 252
                                         10033
 379 ATGGGGCCCATGACCCACTGTACTGGAAAG 10774_
   ATGGGGCCCATGACCC
170 ATGGGGCCCATGACCC----CAGGA---
                                         72861
                                        74452
174
511 ATGGGGCCCATGACCCACTGTACTGGAAAG 156817
215 ATGGGGCCCATGACCCACTGTACTGGAGAG
                                        619856
176 ATGAGGCTC---TCCA----
                                        683480
                                        1291208
541 GAAAACCACTGCGTCTCCTTATCTGGACAC consensus
324
                                        10033
262
  GAAAACCACTGCGTCTCCTTATGTGGACAC 10774
409
185
                                        71854
151
                                        72861
191
       ----CTGC--
174
541 GAAAACCACTGCGTCTCCTTATCTGGACAC 156817
                                        619856
245 GAAAACCA
189 GGAGACCA-
                                        683480
                                - GAGAC 1291208
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571 GTGCAGGCTGGTATTTCAAACCCAGATTT consensus
318
324
                                               10033
252
                                               10644
   GTGCATGCTGGTATTTCAAACCCAGATTT 10774
439
185
                                               71854
151
                                               72861
195
                 -TACTC-
                                               74452
174
                                               155045
571 GTGCAGGCTGGTATTTCAAACCCAGATTT 156817-
224
                                               619856
252
                                               683480
                                            - T 1291208
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501 G C T A T G C G G G C T G T G C T A C A G A G A G T A T G consensus
313 - - - - - - G G G G -
324
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                                                    10644
469 GCTATGCGGGGCTGTGCTACAGAGAGTATG 10774
185
151
                                                   72351
200
        ---CGGNGTTATA--
                                                   74452
174
601 GCTATGCGGGGCTGTGCTACAGAGAGTATG 156817
224
252
208
   GCT-----GGC-----
531 TGCTTTACCAAGCCTGGTGCTGAAGTACCC consensus
                                                   8941
324
                                                   10033
262
                                                   10644
   TGCTTTACCAAGCCTGGTGCTGAAGTACCC 10774
499
185
151
                                                   72861
210
                                             - - C C 74452
174
                                                   155045
631 TGCTTTACCAAGCCTGGTGCTGAAGTACCC 156817
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                                                   619856
252
                                                   683480
214
   -- C T T T -- -
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                                                   1291208
561 A C A G G C A C C A A T G T C C T C T T C C T C C A T C A T consensus
322
324
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262
                                                   10644
529 A C A G G C A C C A A T G T C C T C T T C C T C C A T C A T 10774
185
                                                   71854
151
                                                   72861
219 ATGGGCCCCAAGG-----
                                      --- A C C A C 74452
174
                                                   155045
561 ACAGGCACCAATGTCCTTCCTCCATCAT 156817
224
                                                   619856
252
                                                   683480
224
                       -----CTC----
                                                   1291208
```

```
591 ATAGAGTGCACTCACTCCCCCTGAAAAGCT consensus
322
                                            8941
324
                                            10033
262
                                            10644
   ATAGAGTGCACTCACTCCCCTGAAAAGCT 10774
559
185
                                            71854
151
                                            72861
237 ATG--GTA-ACCAGCTCCTTCTG----CT
                                           74452
174
                                            155045
691 ATAGAGTGCACTCACTCCCCTGAAAGCT
                                           156817
224
                                            619856
252
                                            683480
          TGCAC----CCTCCTGGG---
227
```

```
721 ATCTGAACAGAAGATAATGTAGTGA consensus
 322 ------
                                             8941
 324
                                             10033
 252
 589 ATCTGAACAGAAGATAATGTAGTGA 10774
 151
 259 G C C A G A G C N A C G G C - - - - T G C A A C - - -
 174
    ATCTGAACAGAAGATAATGTAGTGA 156817
 721
 224
                                             619856
 252
                                             683480
 241
                                             1291208
   AGTCCCCATTTGTCCTCAGCCTGTAACTTC consensus
 751
    ----CCCATT
 322
                                             8941
324
                                            10033
252
   AGTCCCCATTTGTTCCTAGNCTGTAACTTC 10774
619
185
                                            71854
151
                                            72861
   ANTGCC--TTTNT----GTCTGTN----C 74452
279
174
751 AGTCCCCATTTGTCCTCAGCCTGTAACTTC 156817
                                            155045
224
                                            619856
252
                                            683480
241
                ---TCTTGG--
                                           -1291208
   CCCGTGTG-CCTATAAAGAAGTTAATAGAG consensus
781
327
                                            8941
324
                                            10033
262
                                            10644
   CC-GTGTGGCCTATAANGAAGTTAATNGNG 10774
649
185
                                            71854
151
                                            72861
  CCT---TGACC-----AATCTNACTGAG 74452
298
174
781 CCCGTGTG-CCTATAAAGAAGTTAATAGAG 156817
224
                                            619856
252
                                            683480
247 - - - G T G C
                                            1291208
```



```
MRLSRRPETFLLAFVLLCTLLGLGCPLHCE GIPL aa MK-----YLHTICLLFIFVARGNSRSCD CNF aa
     ICTAAGSRCHGOMKTCSSDKDTCVLLVGKA GIPL aa
ECHNIGKDCDGYZEECSSPEDVCGKVLLZI CNF aa
    TSKGKELVHTYKGCIRSODCYSGVISTTMG GIPL :
SSASLSVRTVHKNCFSSSICKLGOFDVNIG CNF aa
51
                                                                       GIPL aa
    PKDHMVTSSFCCOSDGCNS-AFLSVPLTNL GIPL : HHSYIRGRINCCEKELCEDOPFPGLPLSK-ONF &&
91
120 TENGLMCPACTASFRDKCMGPMTHCTGKEN GIPL.
113 - PNGYYCPGAIGLFTKDSTEYEAICKGTET CNF 44
                                                                       GIPL aa
150 HCVSLSGHVQAGIFKP--RFAMRGCATESM GIPL aa
142 KCINIVGH-RYEOFPGDISYNLKGCVSS-- CNF aa
178 CFTKPGAEVPTGTNVLFLHHIECTHSP
169 CPLLSLSNATFEONRNYLEKVECKDAIRI
                                                                        GIPL aa
                                                                        CNF aa
204
                                                                        GIPL as
199 S L
                                                                        CNF aa
```

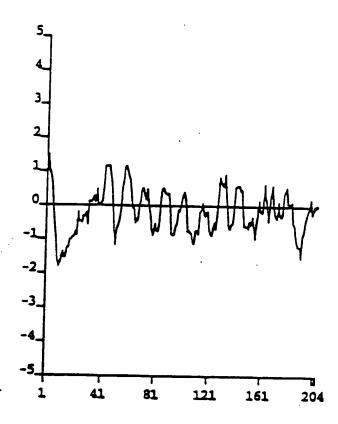


FIGURE 4

